

SEQUENCE LISTING

<110> Cihlar, Tomas

<120> NOVEL GENE ENCODING ORGANIC ANION TRANSPORTER

<130> 240.1PC

<140> unassigned

<141> 1999-06-10

<150> 60/088,864

<151> 1998-06-11

<150> 60/132,267

<151> 1999-05-03

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<170> PatentIn Ver. 2.0

<210> 1

<211> 2123

<212> DNA

<213> Unknown

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<223> Description of Unknown Organism: This information  
is not available.

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<221> CDS

<222> (263)..(1912)

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ggactcagct cccgggaagc aaccagctg cggaggcaac ggcagtgtg ctccctccagc 180

gaaggacagc aggcaggcag acagacagag gtcctggac tggaggcct cagccccag 240

ccactggct gggcctggcc ca atg gcc ttt aat gac ctc ctg cag cag gtg 292

Met Ala Phe Asn Asp Leu Leu Gln Gln Val

1

5

10

ggg ggt gtc ggc cgc ttc cag cag atc cag gtc acc ctg gtg gtc ctc 340

Gly Gly Val Gly Arg Phe Gln Gln Ile Gln Val Thr Leu Val Val Leu

15

20

25

ccc	ctg	ctc	ctg	atg	gct	tct	cac	aac	acc	ctg	cag	aac	ttc	act	gct	388	
Pro	Leu	Leu	Leu	Met	Ala	Ser	His	Asn	Thr	Leu	Gln	Asn	Phe	Thr	Ala		
30									35					40			
gcc	atc	cct	acc	cac	cac	tgc	cgc	ccg	cct	gcc	gat	gcc	aac	ctc	agc	436	
Ala	Ile	Pro	Thr	His	His	Cys	Arg	Pro	Pro	Ala	Asp	Ala	Asn	Leu	Ser		
45									50					55			
aag	aac	ggg	ggg	ctg	gag	gtc	tgg	ctg	ccc	cg	gac	agg	cag	ggg	cag	484	
Lys	Asn	Gly	Gly	Leu	Glu	Val	Trp	Leu	Pro	Arg	Asp	Arg	Gln	Gly	Gln		
60									65					70			
cct	gag	tcc	tgc	ctc	cgc	ttc	acc	tcc	ccg	cag	tgg	gga	ctg	ccc	ttt	532	
Pro	Glu	Ser	Cys	Leu	Arg	Phe	Thr	Ser	Pro	Gln	Trp	Gly	Leu	Pro	Phe		
75									80					85			
ctc	aat	ggc	aca	gaa	gcc	aat	ggc	aca	ggg	gcc	aca	gag	ccc	tgc	acc	580	
Leu	Asn	Gly	Thr	Glu	Ala	Asn	Gly	Thr	Gly	Ala	Thr	Glu	Pro	Cys	Thr		
									95					100			
gat	ggc	tgg	atc	tat	gac	aac	agc	acc	ttc	cca	tct	acc	atc	gtg	act	628	
Asp	Gly	Trp	Ile	Tyr	Asp	Asn	Ser	Thr	Phe	Pro	Ser	Thr	Ile	Val	Thr		
									110					115			
gag	tgg	gac	ctt	gtg	tgc	tct	cac	agg	gcc	cta	cgc	cag	ctg	gcc	cag	676	
Glu	Trp	Asp	Leu	Val	Cys	Ser	His	Arg	Ala	Leu	Arg	Gln	Leu	Ala	Gln		
									125					130			
tcc	ttg	tac	atg	gtg	ggg	gtg	ctg	ctc	gga	gcc	atg	gtg	ttc	ggc	tac	724	
Ser	Leu	Tyr	Met	Val	Gly	Val	Leu	Leu	Gly	Ala	Met	Val	Phe	Gly	Tyr		
									140					145			
ctt	gca	gac	agg	cta	ggc	cgc	cg	aag	gta	ctc	atc	ttg	aac	tac	ctg	772	
Leu	Ala	Asp	Arg	Leu	Gly	Arg	Arg	Lys	Val	Leu	Ile	Leu	Asn	Tyr	Leu		
									155					160			
cag	aca	gct	gtg	tca	ggg	acc	tgc	gca	gcc	ttc	gca	ccc	aac	ttc	ccc	820	
Gln	Thr	Ala	Val	Ser	Gly	Thr	Cys	Ala	Ala	Phe	Ala	Pro	Asn	Phe	Pro		
									175					180			
atc	tac	tgc	gcc	ttc	cg	ctc	tc	tcg	ggc	atg	gct	ctg	gct	ggc	atc	868	
Ile	Tyr	Cys	Ala	Phe	Arg	Leu	Leu	Ser	Gly	Met	Ala	Leu	Ala	Gly	Ile		
									190					195			
tcc	ctc	aac	tgc	atg	aca	ctg	aat	gtg	gag	tgg	atg	ccc	att	cac	aca	916	
Ser	Leu	Asn	Cys	Met	Thr	Leu	Asn	Val	Glu	Trp	Met	Pro	Ile	His	Thr		
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cg	gg	tc	gt	gg	ac	tt	tg	at	gg	ta	gt	ta	ag	ct	gg	ca	964
Arg	Ala	Cys	Val	Gly	Thr	Leu	Ile	Gly	Tyr	Val	Tyr	Ser	Leu	Gly	Gln		
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ttc	ctc	ctg	gct	ggt	gtg	gcc	tac	gct	gtg	ccc	cac	tgg	cgc	cac	ctg	1012
Phe	Leu	Leu	Ala	Gly	Val	Ala	Tyr	Ala	Val	Pro	His	Trp	Arg	His	Leu	
235					240					245					250	
cag	cta	ctg	gtc	tct	gcg	cct	ttt	ttt	gcc	ttc	ttc	atc	tac	tcc	tgg	1060
Gln	Leu	Leu	Val	Ser	Ala	Pro	Phe	Phe	Ala	Phe	Phe	Ile	Tyr	Ser	Trp	
					255					260					265	
ttc	ttc	att	gag	tcg	gcc	cgc	tgg	cac	tcc	tcc	tcc	ggg	agg	ctg	gac	1108
Phe	Phe	Ile	Glu	Ser	Ala	Arg	Trp	His	Ser	Ser	Ser	Gly	Arg	Leu	Asp	
					270					275					280	
ctc	acc	ctg	agg	gcc	ctg	cag	aga	gtc	gcc	cgg	atc	aat	ggg	aag	cgg	1156
Leu	Thr	Leu	Arg	Ala	Leu	Gln	Arg	Val	Ala	Arg	Ile	Asn	Gly	Lys	Arg	
					285					290					295	
gaa	gaa	gga	gcc	aaa	ttg	agt	atg	gag	gta	ctc	cgg	gcc	agt	ctg	cag	1204
Glu	Glu	Gly	Ala	Lys	Leu	Ser	Met	Glu	Val	Leu	Arg	Ala	Ser	Leu	Gln	
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aag	gag	ctg	acc	atg	ggc	aaa	ggc	cag	gca	tcg	gcc	atg	gag	ctg	ctg	1252
Lys	Glu	Leu	Thr	Met	Gly	Lys	Gly	Gln	Ala	Ser	Ala	Met	Glu	Leu	Leu	
					315					320					325	
															330	
cgc	tgc	ccc	acc	ctc	cgc	cac	ctc	ttc	ctc	tgc	ctc	tcc	atg	ctg	tgg	1300
Arg	Cys	Pro	Thr	Leu	Arg	His	Leu	Phe	Leu	Cys	Leu	Ser	Met	Leu	Trp	
					335					340					345	
ttt	gcc	act	agc	ttt	gca	tac	tat	ggg	ctg	gtc	atg	gac	ctg	cag	ggc	1348
Phe	Ala	Thr	Ser	Phe	Ala	Tyr	Tyr	Gly	Leu	Val	Met	Asp	Leu	Gln	Gly	
					350					355					360	
ttt	gga	gtc	agc	atc	tac	cta	atc	cag	gtg	atc	ttt	ggt	gct	gtg	gac	1396
Phe	Gly	Val	Ser	Ile	Tyr	Leu	Ile	Gln	Val	Ile	Phe	Gly	Ala	Val	Asp	
					365					370					375	
ctg	cct	gcc	aag	ctt	gtg	ggc	ttc	ctt	gtc	atc	aac	tcc	ctg	ggt	cgc	1444
Leu	Pro	Ala	Lys	Leu	Val	Gly	Phe	Leu	Val	Ile	Asn	Ser	Leu	Gly	Arg	
					380					385					390	
cgg	cct	gcc	cag	atg	gct	gca	ctg	ctg	gca	ggc	atc	tgc	atc	ctg	1492	
Arg	Pro	Ala	Gln	Met	Ala	Ala	Leu	Leu	Leu	Ala	Gly	Ile	Cys	Ile	Leu	
					395					400					405	
															410	
ctc	aat	ggg	gtg	ata	ccc	cag	gac	cag	tcc	att	gtc	cga	acc	tct	ctt	1540
Leu	Asn	Gly	Val	Ile	Pro	Gln	Asp	Gln	Ser	Ile	Val	Arg	Thr	Ser	Leu	
					415					420					425	
gct	gtg	ctg	ggg	aag	ggt	tgt	ctg	gct	gcc	tcc	ttc	aac	tgc	atc	tcc	1588
Ala	Val	Leu	Gly	Lys	Gly	Cys	Leu	Ala	Ala	Ser	Phe	Asn	Cys	Ile	Phe	
					430					435					440	

ctg tat act ggg gaa ctg tat ccc aca atg atc cg<sup>g</sup> cag aca ggc atg 1636  
 Leu Tyr Thr Gly Glu Leu Tyr Pro Thr Met Ile Arg Gln Thr Gly Met  
 445 450 455

gga atg ggc agc acc atg gcc cga gtg ggc agc atc gtg agc cca ctg 1684  
 Gly Met Gly Ser Thr Met Ala Arg Val Gly Ser Ile Val Ser Pro Leu  
 460 465 470

gtg agc atg act gcc gag ctc tac ccc tcc atg cct ctc ttc atc tac 1732  
 Val Ser Met Thr Ala Glu Leu Tyr Pro Ser Met Pro Leu Phe Ile Tyr  
 475 480 485 490

ggt gct gtt cct gtg gcc gcc agc gct gtc act gtc ctc ctg cca gag 1780  
 Gly Ala Val Pro Val Ala Ala Ser Ala Val Thr Val Leu Leu Pro Glu  
 495 500 505

acc ctg ggc cag cca ctg cca gac acg gtg cag gac ctg gag agc agg 1828  
 Thr Leu Gly Gln Pro Leu Pro Asp Thr Val Gln Asp Leu Glu Ser Arg  
 510 515 520

aaa ggg aaa cag acg cga cag caa caa gag cac cag aag tat atg gtc 1876  
 Lys Gly Lys Gln Thr Arg Gln Gln Glu His Gln Lys Tyr Met Val  
 525 530 535

cca ctg cag gcc tca gca caa gag aag aat gga ctc tgaggactga 1922  
 Pro Leu Gln Ala Ser Ala Gln Glu Lys Asn Gly Leu  
 540 545 550

gaagggggcct tacagaaccc taaagggagg gaaggtccta caggtctccg gccacccaca 1982

caaggaggag gaagagggaaa tggtgaccca agtgtgggg ttgtggttca ggaaagcatc 2042

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ctgcgaaaaaa aaaaaaaaaa a 2123

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<212> PRT

<213> Unknown

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 20 25 30

Ser His Asn Thr Leu Gln Asn Phe Thr Ala Ala Ile Pro Thr His His  
 35 40 45

Cys Arg Pro Pro Ala Asp Ala Asn Leu Ser Lys Asn Gly Gly Leu Glu  
50 55 60

Val Trp Leu Pro Arg Asp Arg Gln Gly Gln Pro Glu Ser Cys Leu Arg  
65 70 75 80

Phe Thr Ser Pro Gln Trp Gly Leu Pro Phe Leu Asn Gly Thr Glu Ala  
85 90 95

Asn Gly Thr Gly Ala Thr Glu Pro Cys Thr Asp Gly Trp Ile Tyr Asp  
100 105 110

Asn Ser Thr Phe Pro Ser Thr Ile Val Thr Glu Trp Asp Leu Val Cys  
115 120 125

Ser His Arg Ala Leu Arg Gln Leu Ala Gln Ser Leu Tyr Met Val Gly  
130 135 140

Val Leu Leu Gly Ala Met Val Phe Gly Tyr Leu Ala Asp Arg Leu Gly  
145 150 155 160

Arg Arg Lys Val Leu Ile Leu Asn Tyr Leu Gln Thr Ala Val Ser Gly  
165 170 175

Thr Cys Ala Ala Phe Ala Pro Asn Phe Pro Ile Tyr Cys Ala Phe Arg  
180 185 190

Leu Leu Ser Gly Met Ala Leu Ala Gly Ile Ser Leu Asn Cys Met Thr  
195 200 205

Leu Asn Val Glu Trp Met Pro Ile His Thr Arg Ala Cys Val Gly Thr  
210 215 220

Leu Ile Gly Tyr Val Tyr Ser Leu Gly Gln Phe Leu Leu Ala Gly Val  
225 230 235 240

Ala Tyr Ala Val Pro His Trp Arg His Leu Gln Leu Leu Val Ser Ala  
245 250 255

Pro Phe Phe Ala Phe Phe Ile Tyr Ser Trp Phe Phe Ile Glu Ser Ala  
260 265 270

Arg Trp His Ser Ser Ser Gly Arg Leu Asp Leu Thr Leu Arg Ala Leu  
275 280 285

Gln Arg Val Ala Arg Ile Asn Gly Lys Arg Glu Glu Gly Ala Lys Leu  
290 295 300

Ser Met Glu Val Leu Arg Ala Ser Leu Gln Lys Glu Leu Thr Met Gly  
305 310 315 320

Lys Gly Gln Ala Ser Ala Met Glu Leu Leu Arg Cys Pro Thr Leu Arg  
325 330 335

His Leu Phe Leu Cys Leu Ser Met Leu Trp Phe Ala Thr Ser Phe Ala  
340 345 350

Tyr Tyr Gly Leu Val Met Asp Leu Gln Gly Phe Gly Val Ser Ile Tyr  
355 360 365

Leu Ile Gln Val Ile Phe Gly Ala Val Asp Leu Pro Ala Lys Leu Val  
370 375 380

Gly Phe Leu Val Ile Asn Ser Leu Gly Arg Arg Pro Ala Gln Met Ala  
385 390 395 400

Ala Leu Leu Leu Ala Gly Ile Cys Ile Leu Leu Asn Gly Val Ile Pro  
405 410 415

Gln Asp Gln Ser Ile Val Arg Thr Ser Leu Ala Val Leu Gly Lys Gly  
420 425 430

Cys Leu Ala Ala Ser Phe Asn Cys Ile Phe Leu Tyr Thr Gly Glu Leu  
435 440 445

Tyr Pro Thr Met Ile Arg Gln Thr Gly Met Gly Met Gly Ser Thr Met  
450 455 460

Ala Arg Val Gly Ser Ile Val Ser Pro Leu Val Ser Met Thr Ala Glu  
465 470 475 480

Leu Tyr Pro Ser Met Pro Leu Phe Ile Tyr Gly Ala Val Pro Val Ala  
485 490 495

Ala Ser Ala Val Thr Val Leu Leu Pro Glu Thr Leu Gly Gln Pro Leu  
500 505 510

Pro Asp Thr Val Gln Asp Leu Glu Ser Arg Lys Gly Lys Gln Thr Arg  
515 520 525

Gln Gln Gln Glu His Gln Lys Tyr Met Val Pro Leu Gln Ala Ser Ala  
530 535 540

Gln Glu Lys Asn Gly Leu  
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<211> 77  
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<213> Unknown

<220>

<223> Description of Unknown Organism:This information is not available.

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<210> 4  
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<212> DNA  
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<212> DNA  
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<220>  
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<212> DNA

<213> Unknown

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<223> Description of Unknown Organism:This information  
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<212> PRT

<213> Unknown

<220>

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is not available.

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